



#6

-54-

SEQUENCE LISTING

(1)

GENERAL INFORMATION:

(i) APPLICANT: HUMAN GENOME SCIENCES, INC.  
9410 KEY WEST AVENUE  
ROCKVILLE, MD 20850  
UNITED STATES OF AMERICA

APPLICANTS/INVENTORS: LI, YI  
CAO, LIANG  
ROSEN, CRAIG A.

(ii) TITLE OF INVENTION: Human G-Protein Coupled Receptor

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
(B) STREET: 1100 NEW YORK AVE., NW, SUITE 600  
(C) CITY: WASHINGTON  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: FLOPPY DISK  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US95/04079  
(B) FILING DATE: 30-MAR-1995  
(C) CLASSIFICATION:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/765,973  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: STEFFE, ERIC K.  
(B) REGISTRATION NUMBER: 36,688  
(C) REFERENCE/DOCKET NUMBER: 1488.114PC00/EKS/KLM

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1713 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 116..1003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGT CATTCAACAT TTATTCAACC AAAAATACTA AGTCAGCTCT ATACAAACTA	60
ATGGAAGGAT ACAGCTATGC AAATATAGAA CACTAAAGTG TTACATGACA GATGT ATG	118
	Met
	1
AGT AGT GAA ATG GTG AAA AAT CAG ACA ATG GTC ACA GAG TTC CTC CTA	166
Ser Ser Glu Met Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu	
	5 10 15
CTG GGA TTT CTC CTG GGC CCA AGG ATT CAG ATG CTC CTC TTT GGG CTC	214
Leu Gly Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu	
	20 25 30
TTC TCC CTG TTC TAT GTC TTC ACC CTG CTG GGG AAT GGG ACC ATC CTG	262
Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu	
	35 40 45
GGG CTC ATC TCA CTG GAC TCC AGA CTC CAC ACC CCC ATG TAC TTC TTC	310
Gly Leu Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe	
	50 55 60 65
CTC TCA CAC CTG GCC GTC GTC AAC ATC GCC TAT GCC TGC AAC ACA GTG	358
Leu Ser His Leu Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val	
	70 75 80
CCC CAG ATG CTG GTG AAC CTC CTG CAT CCA GCC AAG CCC ATC TCC TTT	406
Pro Gln Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe	
	85 90 95
GCT GGT TGC ATG ACA CTA GAC TTT CTC TTT TTG AGT TTT GCA CAT ACT	454
Ala Gly Cys Met Thr Leu Asp Phe Leu Phe Leu Ser Phe Ala His Thr	
	100 105 110
GAA TGC CTC CTG TTG GTG CTG ATG TCC TAC GAT CGG TAC GTG GCC ATC	502
Glu Cys Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile	
	115 120 125
TGC CAC CCT CTC CGA TAT TTC ATC ATC ATG ACC TGG AAA GTC TGC ATC	550
Cys His Pro Leu Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile	
	130 135 140 145
ACT CTG GGC ATC ACT TCC TGG ACA TGT GGC TCC CTC CTG GCT ATG GTC	598
Thr Leu Gly Ile Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val	
	150 155 160
CAT GTG AGC CTC ATC CTA AGA CTG CCC TTT TGT GGG CCT CGT GAA ATC	646
His Val Ser Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile	
	165 170 175
AAC CAC TTC TTC TGT GAA ATC CTG TCT GTC CTC AGG CTG GCC TGT GCT	694
Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala	
	180 185 190
GAT ACC TGG CTC AAC CAG GTG GTC ATC TTT GAA GCC TGC ATG TTC ATC	742

Asp	Thr	Trp	Leu	Asn	Gln	Val	Val	Ile	Phe	Glu	Ala	Cys	Met	Phe	Ile	
195						200					205					
CTG	GTG	GGA	CCA	CTC	TGC	CTG	GTG	CTG	GTC	TCC	TAC	TCA	CAC	ATC	CTG	790
Leu	Val	Gly	Pro	Leu	Cys	Leu	Val	Leu	Val	Ser	Tyr	Ser	His	Ile	Leu	
210					215					220					225	
GGG	GGC	ATC	CTG	AGG	ATC	CAG	TCT	GGG	GAG	GGC	CGC	AGA	AAG	GCC	TTC	838
Gly	Gly	Ile	Leu	Arg	Ile	Gln	Ser	Gly	Glu	Gly	Arg	Arg	Lys	Ala	Phe	
				230					235					240		
TCC	ACC	TGC	TCC	TCC	CAC	CTC	TGC	GTA	GTG	GGA	CTC	TTC	TTT	GGG	AGC	886
Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Phe	Gly	Ser	
			245					250					255			
GCC	ATC	GTC	ATG	TAC	ATG	GCC	CCT	AAG	TCC	CGC	CAT	CCT	GAG	GAG	CAG	934
Ala	Ile	Val	Met	Tyr	Met	Ala	Pro	Lys	Ser	Arg	His	Pro	Glu	Glu	Gln	
		260					265					270				
CAG	AAG	GTC	CTT	TTT	CTT	ATT	TTA	CAG	TTC	CTT	TCA	ACC	CCG	ATG	CTT	982
Gln	Lys	Val	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Leu	Ser	Thr	Pro	Met	Leu	
	275					280					285					
AAA	CCC	CCT	GAT	TTA	CAA	CCC	TGA	GGAATGTAGA	GGGTCAAGGG	TGCCCTCCGA						1036
Lys	Pro	Pro	Asp	Leu	Gln	Pro										
290					295											
GGAGACCACT	GTGCAARGRA	AGTCATTCCT	AAGGGGTGTG	ACATTTGAAC	TGCCAGCCCC											1096
AGTTGCCCCG	TGGAATCCTG	ATGCCCAATT	ATTGCCTCAA	CCCAGAAAAG	TTTACTCCCC											1156
TTTAACTGTG	CTTTACTGAC	AGAAGGGCAA	GCCTTCTCCC	GTTTTTTGCA	GATAAAATTT											1216
TAGATGTGTT	GCAATCATTG	GGTTTCTAGG	AGATGTGGTT	TTATCAGACA	ATTTTTTCTT											1276
TTATTTTACA	ATTACTTTAA	TATCTGTAAA	ATAAAGAATT	ATTTTAAATC	ATTTTCCCAG											1336
TCCCAAAAGT	TAAATACAGG	CCACTTACTT	CTTTAACCAA	ATGATATAGT	TTGGCTCTGT											1396
GTCCCCACCC	AAATCTCATG	TCAAATTGTA	ATCCCCGCAT	GTCAGCGGAG	GGACCTGGTG											1456
GGAGGTGATT	GGATCATGGG	GAGGGATTTC	CCCCTTGCTG	TTCTGTTGAT	AGTGAACGAG											1516
TTCTCACGAA	ATCTGATGGT	TTAAAAGTGC	AGCACTTCTC	CCTTTGCTCT	CTCTCTCCTG											1576
CTGTGCCATG	GTAAGACGTG	CCTTGCTTCC	CCTGGTGCTT	CCGCCATGAT	TGTACCTTTC											1636
CTGAGGCCTC	TCCAGCCATG	TGGAAGTGTG	AGCCAATTAA	ACTTCTTTTC	TTTAGAAAAA											1696
AAAAAAAAAA	AAAAAAA															1713

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Glu	Met	Val	Lys	Asn	Gln	Thr	Met	Val	Thr	Glu	Phe	Leu
1				5					10					15	
Leu	Leu	Gly	Phe	Leu	Leu	Gly	Pro	Arg	Ile	Gln	Met	Leu	Leu	Phe	Gly
			20					25					30		
Leu	Phe	Ser	Leu	Phe	Tyr	Val	Phe	Thr	Leu	Leu	Gly	Asn	Gly	Thr	Ile
		35					40					45			
Leu	Gly	Leu	Ile	Ser	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe
	50					55					60				
Phe	Leu	Ser	His	Leu	Ala	Val	Val	Asn	Ile	Ala	Tyr	Ala	Cys	Asn	Thr
65					70					75					80
Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Leu	His	Pro	Ala	Lys	Pro	Ile	Ser
				85					90					95	
Phe	Ala	Gly	Cys	Met	Thr	Leu	Asp	Phe	Leu	Phe	Leu	Ser	Phe	Ala	His
			100					105					110		
Thr	Glu	Cys	Leu	Leu	Leu	Val	Leu	Met	Ser	Tyr	Asp	Arg	Tyr	Val	Ala
		115					120					125			
Ile	Cys	His	Pro	Leu	Arg	Tyr	Phe	Ile	Ile	Met	Thr	Trp	Lys	Val	Cys
	130					135					140				
Ile	Thr	Leu	Gly	Ile	Thr	Ser	Trp	Thr	Cys	Gly	Ser	Leu	Leu	Ala	Met
145					150					155					160
Val	His	Val	Ser	Leu	Ile	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Pro	Arg	Glu
				165					170					175	
Ile	Asn	His	Phe	Phe	Cys	Glu	Ile	Leu	Ser	Val	Leu	Arg	Leu	Ala	Cys
			180					185					190		
Ala	Asp	Thr	Trp	Leu	Asn	Gln	Val	Val	Ile	Phe	Glu	Ala	Cys	Met	Phe
		195					200					205			
Ile	Leu	Val	Gly	Pro	Leu	Cys	Leu	Val	Leu	Val	Ser	Tyr	Ser	His	Ile
	210					215					220				
Leu	Gly	Gly	Ile	Leu	Arg	Ile	Gln	Ser	Gly	Glu	Gly	Arg	Arg	Lys	Ala
225					230					235					240
Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Phe	Gly
				245					250					255	
Ser	Ala	Ile	Val	Met	Tyr	Met	Ala	Pro	Lys	Ser	Arg	His	Pro	Glu	Glu
			260					265					270		
Gln	Gln	Lys	Val	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Leu	Ser	Thr	Pro	Met
		275					280					285			
Leu	Lys	Pro	Pro	Asp	Leu	Gln	Pro								
	290					295									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 884..2062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TC	ACT	TAG	AGG	GCG	AAT	TGG	TAC	GGG	CCCC	CCCT	CGAG	GT	CGAC	GGT	ATC	GATA	AGCT	TG	60	
AT	ATC	GAA	TT	CGG	CAC	GAG	CGG	GCT	CGGA	GAG	GT	GAC	CGG	AAC	CGGG	GCT	GGTA	GCA	TAG	120
TT	TGA	TTT	TGA	TG	ATG	GAG	CC	AAC	ACAG	GGG	TTG	GAG	CT	TG	TAC	CGGT	GAA	GCT	GAG	180
AAA	AGG	TT	CC	TG	GAG	TAG	AC	GAT	GG	AG	CCA	TAA	CT	GGA	AC	CGG	AGT	CT	GT	240
AGG	AC	AGG	AG	CAG	CAC	CT	TGG	CG	ATG	GT	GCC	AGG	ACC	GG	AA	GAG	GAG	CC	AG	300
GG	AG	AAG	GAG	CC	AGA	AAT	TGC	TGT	CT	GT	TGA	GCC	GCC	AT	AG	GAG	CC	AG	AG	360
GC	CT	GAG	AAT	GC	AGA	AAT	GC	CT	GG	AG	CC	AG	AAG	GA	AG	CC	TG	AG	CT	420
TG	CT	GAC	CG	AA	AGG	ACT	TGG	CC	AG	AG	CC	GA	AG	CT	TGG	CACC	AGG	GAC	AG	480
GGG	CC	AC	CGG	TG	AG	TT	CA	AC	CC	ACT	GACT	T	CAG	GT	GA	AGG	ACT	GT	GG	540
GAG	GC	CT	CAC	CAG	AG	TGGG	T	GT	GGG	G	CAT	G	GGG	G	CT	CG	AG	TAC	CC	600
GG	TAG	CCCC	GG	CC	AGG	GG	TTA	ACG	TGGG	G	CG	TGG	ATT	CA	AC	AG	CT	TG	GA	660
TC	GG	AGG	CCC	GGG	TG	CT	TGG	GCC	AAT	TG	AG	GA	AC	AGG	AGT	C	AG	TCC	AT	720
GT	CT	CAC	TAC	AAT	CT	T	CACA	CG	CCT	T	TATT	ATT	CAC	CA	TG	G	TTG	G	T	780
AG	CA	AG	CG	GA	AGG	CT	GAG	GC	CAG	TAG	GGG	G	AGG	GT	G	T	CTG	G	G	840
CAC	AG	AG	ACA	GGG	G	TAG	GGG	CAG	GGG	G	T	CGG	GG	CC	AC	GG	CC	TGG	ATG	895
																		Met	Arg	
																		1		
TGG	GCA	GGC	TGG	CTG	ATG	AGA	TGG	TGC	TGC	CCC	CCT	GCT	GAC	ACG	AGG					943
Trp	Ala	Gly	Trp	Leu	Met	Arg	Trp	Cys	Cys	Pro	Pro	Ala	Asp	Thr	Arg					
5					10					15					20					
TGC	ACC	ACA	TTC	CTT	TGC	AGC	GGG	CGG	GCT	GCC	CCA	CAG	CAA	GCT	GGC					991
Cys	Thr	Thr	Phe	Leu	Cys	Ser	Gly	Arg	Ala	Ala	Pro	Gln	Gln	Ala	Gly					
				25					30						35					
GCA	CCT	GGG	CAC	CAT	CCA	AAA	TAC	AGC	TTG	TTT	CCC	TGG	ATT	TGG	AAG					1039
Ala	Pro	Gly	His	His	Pro	Lys	Tyr	Ser	Leu	Phe	Pro	Trp	Ile	Trp	Lys					
			40					45						50						
GTG	AGA	GGT	TTG	CTT	CCC	CCT	CCA	TTA	ACC	ACT	GAC	GTT	GTG	CCA	GTG					1087
Val	Arg	Gly	Leu	Leu	Pro	Pro	Pro	Leu	Thr	Thr	Asp	Val	Val	Pro	Val					
			55					60						65						
AGA	CTA	ACT	CTC	CGC	GCC	AAT	CTG	TCC	GCG	GCT	GAC	CTC	CTT	CGC	GGG					1135

Arg	Leu	Thr	Leu	Arg	Ala	Asn	Leu	Ser	Ala	Ala	Asp	Leu	Leu	Arg	Gly	
	70					75					80					
CGT	GGC	CTA	CCT	CTT	CCT	CAT	GTT	CCA	CAC	TGT	CCC	CGC	ACA	GCC	CGA	1183
Arg	Gly	Leu	Pro	Leu	Pro	His	Val	Pro	His	Cys	Pro	Arg	Thr	Ala	Arg	
	85				90					95					100	
CTT	TCA	CTT	GAG	GGC	TGG	TTC	CTG	CGG	CAG	GGC	TTG	CTG	GAC	ACA	AAC	1231
Leu	Ser	Leu	Glu	Gly	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Thr	Asn	
				105					110					115		
CTC	ACT	GCG	TCG	GTG	GCC	ACA	CTG	CTG	GCC	ATC	GCC	GTG	GAG	CGG	CAC	1279
Leu	Thr	Ala	Ser	Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala	Val	Glu	Arg	His	
			120				125						130			
CGC	AGT	GTG	ATG	GCC	GTG	CAG	CTG	CAC	AGC	CGC	CTG	CCC	CGT	GGC	CGC	1327
Arg	Ser	Val	Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu	Pro	Arg	Gly	Arg	
		135					140					145				
GTG	GTC	ATG	CTC	ATT	GTG	GGC	GTG	TGG	GTG	GCT	GCC	CTG	GGC	CTG	GGG	1375
Val	Val	Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	Leu	Gly	Leu	Gly	
	150					155					160					
CTG	CTG	CCT	GCC	CAC	TCC	TGG	CAC	TGC	CTC	TGT	GCC	CTG	GAC	CGC	TCC	1423
Leu	Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala	Leu	Asp	Arg	Ser	
	165				170					175					180	
TCA	CGC	ATG	GCA	CCC	CTG	CTC	AGC	CGC	TCC	TAT	TTG	GCC	GTC	TGG	GCT	1471
Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu	Ala	Val	Trp	Ala	
				185					190					195		
CTG	TCG	AGC	CTG	CTT	GTC	TTC	CTG	CTC	ATG	GTG	GCT	GTG	TAC	ACC	CGC	1519
Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala	Val	Tyr	Thr	Arg	
			200					205					210			
ATT	TTC	TTC	TAC	GTG	CGG	CGG	CGA	GTG	CAG	CGC	ATG	GCA	GAG	CAT	GTC	1567
Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met	Ala	Glu	His	Val	
		215					220					225				
AGC	TGC	CAC	CCC	CGC	TAC	CGA	GAG	ACC	ACG	CTC	AGC	CTG	GTC	AAG	ACT	1615
Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser	Leu	Val	Lys	Thr	
	230					235					240					
GTT	GTC	ATC	ATC	CTG	GGG	GCG	TTC	GTG	GTC	TGC	TGG	ACA	CCA	GGC	CAG	1663
Val	Val	Ile	Ile	Leu	Gly	Ala	Phe	Val	Val	Cys	Trp	Thr	Pro	Gly	Gln	
	245				250					255					260	
GTG	GTA	CTG	CTC	CTG	GAT	GGT	TTA	GGC	TGT	GAG	TCC	TGC	AAT	GTC	CTG	1711
Val	Val	Leu	Leu	Leu	Asp	Gly	Leu	Gly	Cys	Glu	Ser	Cys	Asn	Val	Leu	
				265					270					275		
GCG	TTA	GAA	AAG	TAC	TTC	CTA	CTG	TTG	GCC	GAG	CCA	ACC	TCA	CTG	GTC	1759
Ala	Leu	Glu	Lys	Tyr	Phe	Leu	Leu	Leu	Ala	Glu	Pro	Thr	Ser	Leu	Val	
			280					285					290			
AAT	GCT	GCT	GTG	TAC	TCT	TGC	CGA	GAT	GCT	GAG	ATG	CGC	CGC	ACC	TTC	1807
Asn	Ala	Ala	Val	Tyr	Ser	Cys	Arg	Asp	Ala	Glu	Met	Arg	Arg	Thr	Phe	
		295					300					305				
CGC	CGC	CTT	CTC	CTG	CTG	CGC	GTG	CCT	CCG	CCA	GTC	CAC	CCG	CGA	GTC	1855
Arg	Arg	Leu	Leu	Leu	Leu	Arg	Val	Pro	Pro	Pro	Val	His	Pro	Arg	Val	
	310					315					320					

TGT	CCA	CTA	TAC	ATC	CTC	TGC	CCA	GGG	AGG	TGC	CAG	CAC	TCG	CAT	CAT	1903
Cys	Pro	Leu	Tyr	Ile	Leu	Cys	Pro	Gly	Arg	Cys	Gln	His	Ser	His	His	
325					330					335					340	
GCT	TCC	CGA	GAA	CGG	CCA	CCC	ACT	GAT	GGA	CTC	CAC	CCT	TTA	GCT	ACC	1951
Ala	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Asp	Gly	Leu	His	Pro	Leu	Ala	Thr	
				345					350					355		
TTG	AAC	TAC	AGC	GGT	ACG	CGG	CAA	GCA	ACA	AAT	CCA	CAG	CCC	CTG	ATG	1999
Leu	Asn	Tyr	Ser	Gly	Thr	Arg	Gln	Ala	Thr	Asn	Pro	Gln	Pro	Leu	Met	
			360					365					370			
ACT	TGT	GGG	TGC	TCC	TGG	CTC	AAC	CCA	ACC	TCG	TGC	CGA	ATT	CCT	GCA	2047
Thr	Cys	Gly	Cys	Ser	Trp	Leu	Asn	Pro	Thr	Ser	Cys	Arg	Ile	Pro	Ala	
		375					380					385				
GCC	CGG	GGG	ATC	CAC	TAG	TTCTAGAGCG	GCGCCACCGC	GGTGGAGCTC								2095
Ala	Arg	Gly	Ile	His												
		390														
CAGCTTTTGT TCCCTTTAGT GAGGGTTAAT TTCGAGCTTG GCGTAATCAT GGTCATAGCT															2155	
GTTTCCTGTG TGAAATTGTT ATCCGCTCAC															2185	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Pro	Thr	Trp	Ala	Gly	Trp	Leu	Met	Arg	Trp	Cys	Cys	Pro	Pro
1				5					10					15	
Ala	Asp	Thr	Arg	Cys	Thr	Thr	Phe	Leu	Cys	Ser	Gly	Arg	Ala	Ala	Pro
			20					25					30		
Gln	Gln	Ala	Gly	Ala	Pro	Gly	His	His	Pro	Lys	Tyr	Ser	Leu	Phe	Pro
		35				40						45			
Trp	Ile	Trp	Lys	Val	Arg	Gly	Leu	Leu	Pro	Pro	Pro	Leu	Thr	Thr	Asp
	50					55					60				
Val	Val	Pro	Val	Arg	Leu	Thr	Leu	Arg	Ala	Asn	Leu	Ser	Ala	Ala	Asp
	65				70					75					80
Leu	Leu	Arg	Gly	Arg	Gly	Leu	Pro	Leu	Pro	His	Val	Pro	His	Cys	Pro
				85				90						95	
Arg	Thr	Ala	Arg	Leu	Ser	Leu	Glu	Gly	Trp	Phe	Leu	Arg	Gln	Gly	Leu
		100						105					110		
Leu	Asp	Thr	Asn	Leu	Thr	Ala	Ser	Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala
		115					120					125			
Val	Glu	Arg	His	Arg	Ser	Val	Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu
	130					135					140				



Pro	Arg	Gly	Arg	Val	Val	Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	145	150	155				160
Leu	Gly	Leu	Gly	Leu	Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala		165	170				175
Leu	Asp	Arg	Ser	Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu		180	185				190
Ala	Val	Trp	Ala	Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala		195	200				205
Val	Tyr	Thr	Arg	Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met		210	215				220
Ala	Glu	His	Val	Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser		225	230				240
Leu	Val	Lys	Thr	Val	Val	Ile	Ile	Leu	Gly	Ala	Phe	Val	Val	Cys	Trp		245	250				255
Thr	Pro	Gly	Gln	Val	Val	Leu	Leu	Leu	Asp	Gly	Leu	Gly	Cys	Glu	Ser		260	265				270
Cys	Asn	Val	Leu	Ala	Leu	Glu	Lys	Tyr	Phe	Leu	Leu	Leu	Ala	Glu	Pro		275	280				285
Thr	Ser	Leu	Val	Asn	Ala	Ala	Val	Tyr	Ser	Cys	Arg	Asp	Ala	Glu	Met		290	295				300
Arg	Arg	Thr	Phe	Arg	Arg	Leu	Leu	Leu	Leu	Arg	Val	Pro	Pro	Pro	Val		305	310				320
His	Pro	Arg	Val	Cys	Pro	Leu	Tyr	Ile	Leu	Cys	Pro	Gly	Arg	Cys	Gln		325	330				335
His	Ser	His	His	Ala	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Asp	Gly	Leu	His		340	345				350
Pro	Leu	Ala	Thr	Leu	Asn	Tyr	Ser	Gly	Thr	Arg	Gln	Ala	Thr	Asn	Pro		355	360				365
Gln	Pro	Leu	Met	Thr	Cys	Gly	Cys	Ser	Trp	Leu	Asn	Pro	Thr	Ser	Cys		370	375				380
Arg	Ile	Pro	Ala	Ala	Arg	Gly	Ile	His								385	390					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 62..940



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCACGAGC ATAAGAAGAC AGAGAGAACT GAGTATCCTC CCAAAGGTGA CACTGGAAGC	60
A ATG AAC ACC ACA GTA ATG CAA GGC TTC AAC AGA TCT AAG CGG TGC	106
Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Lys Arg Cys	
1 5 10 15	
CCC AAA GAC ACT CGG ATA GTA CAG CTG GTA TTC CCA GCC CTC TAC ACA	154
Pro Lys Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr	
20 25 30	
GTG GTT TTC TTG ACC GGA ATC CTG CTG AAT ACT TTG GCT CTG TGG GTG	202
Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val	
35 40 45	
TTT GTT CAC ATC CCC AGC TCC TCC ACC TTC ATC ATC TAC CTC AAA AAC	250
Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn	
50 55 60	
ACT TTG GTG GCC GAC TTG ATA ATG ACA CTC ATG CTT CCT TTC AAA ATC	298
Thr Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile	
65 70 75	
CTC TCT GAC TCA CAC CTG GCA CCC TGG CAG CTC AGA GCT TTT GTG TGT	346
Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys	
80 85 90 95	
CGT TTT TCT TCG GTG ATA TTT TAT GAG ACC ATG TAT GTG GGC ATC GTG	394
Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val	
100 105 110	
CTG TTA GGG CTC ATA GCC TTT GAC AGA TTC CTC AAG ATC ATC AGA CCT	442
Leu Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro	
115 120 125	
TTG AGA AAT ATT TTT CTA AAA AAA CCT GTT TGG GGA AAA ACG GTC TCA	490
Leu Arg Asn Ile Phe Leu Lys Lys Pro Val Trp Gly Lys Thr Val Ser	
130 135 140	
ATC TTC ATC TGG TTC TTT TGG TTC TTC ATC TCC CTG CCA AAT ATG ATC	538
Ile Phe Ile Trp Phe Phe Trp Phe Phe Ile Ser Leu Pro Asn Met Ile	
145 150 155	
TTG AGC AAC AAG GAA GCA ACA CCA TCG TCT GTG AAA AAG TGT GCT TCC	586
Leu Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser	
160 165 170 175	
TTA AAG GGG CCT CTG GGG CTG AAA TGG CAT CAA ATG GTA AAT AAC ATA	634
Leu Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile	
180 185 190	
TGC CAG TTT ATT TTC TGG ACT GTT TTT ATC CTA ATG CTT GTG TTT TAT	682
Cys Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr	
195 200 205	
GTG GTT ATT GCA AAA AAG TAT ATG ATT CTT ATA GAA AGT CCA AAA GTA	730
Val Val Ile Ala Lys Lys Tyr Met Ile Leu Ile Glu Ser Pro Lys Val	
210 215 220	
AGG ACA GAA AAA ACA ACA AAA AGC TGG AAG GCA AAG TAT TTG TTG TCG	778

Arg	Thr	Glu	Lys	Thr	Thr	Lys	Ser	Trp	Lys	Ala	Lys	Tyr	Leu	Leu	Ser	
225						230					235					
TGG	CTG	TCT	TCT	TTG	TGT	GTT	TTG	CTC	CAT	TTC	ATT	TCG	CCA	GAG	TTC	826
Trp	Leu	Ser	Ser	Leu	Cys	Val	Leu	Leu	His	Phe	Ile	Ser	Pro	Glu	Phe	
240					245					250					255	
CAT	ATA	CTC	ACA	GTC	AAA	CCA	ACA	ATA	AGA	CTG	ACT	GTA	GAC	TGC	AAA	874
His	Ile	Leu	Thr	Val	Lys	Pro	Thr	Ile	Arg	Leu	Thr	Val	Asp	Cys	Lys	
				260					265					270		
ATC	AAC	TGT	TTA	TTG	CTA	AAG	AAA	CAA	CTC	TCT	TTT	TGG	CAG	CAA	CTA	922
Ile	Asn	Cys	Leu	Leu	Leu	Lys	Lys	Gln	Leu	Ser	Phe	Trp	Gln	Gln	Leu	
			275					280					285			
ACA	TTT	GTA	TGG	ATC	CCT	TAA	TATACATATT	CTTATGTAAA	AAATTCACAG							973
Thr	Phe	Val	Trp	Ile	Pro											
			290													
AAAAGCTACC	ATGTATGCAA	GGGAGAAAGA	CCACAGCATC	AAGCCAAGAA	AATCATAGCA											1033
GTCAGACAGA	CAACATAACC	TTAGGCTGAC	AACTGTACAT	AGGGGTAACT	TCTATTTATT											1093
GATGAGACTT	CCGTAGATAA	TGTGGAAATC	CAATTTAACC	AAGAAAAAAA	GATTGGGGCA											1153
AATGCTCTCT	TACATTTTAT	TATCCTGGTG	TACAGAAAAG	ATTATATAAA	ATTTAAATCC											1213
ACATAGATCT	ATTCATAAGC	TGAATGAACC	ATTACTAAGA	GAATGCAACA	GGATACAAAT											1273
GGCCACTAGA	GGTCATTATT	TCTTTCTTTC	TTTCTTTTTT	TTTTTTTAAT	TTCAAGAGCA											1333
TTTCACTTTA	ACATTTTGGA	AAAGACTAAG	GAGAAACGTA	TATCCCTACA	AACCTCCCCT											1393
CCAAACACCT	TCTTACATTC	TTTTCCACAA	TTCACATAAC	ACTACTGCTT	TTGTGCCCCT											1453
TAAATGTAGA	TTTGTTGGCT	G														1474

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Lys	Arg	Cys	Pro
1				5					10					15	
Lys	Asp	Thr	Arg	Ile	Val	Gln	Leu	Val	Phe	Pro	Ala	Leu	Tyr	Thr	Val
			20					25					30		
Val	Phe	Leu	Thr	Gly	Ile	Leu	Leu	Asn	Thr	Leu	Ala	Leu	Trp	Val	Phe
		35				40						45			
Val	His	Ile	Pro	Ser	Ser	Ser	Thr	Phe	Ile	Ile	Tyr	Leu	Lys	Asn	Thr
	50					55					60				
Leu	Val	Ala	Asp	Leu	Ile	Met	Thr	Leu	Met	Leu	Pro	Phe	Lys	Ile	Leu

65		70		75		80									
Ser	Asp	Ser	His	Leu	Ala	Pro	Trp	Gln	Leu	Arg	Ala	Phe	Val	Cys	Arg
			85						90					95	
Phe	Ser	Ser	Val	Ile	Phe	Tyr	Glu	Thr	Met	Tyr	Val	Gly	Ile	Val	Leu
			100					105					110		
Leu	Gly	Leu	Ile	Ala	Phe	Asp	Arg	Phe	Leu	Lys	Ile	Ile	Arg	Pro	Leu
		115					120					125			
Arg	Asn	Ile	Phe	Leu	Lys	Lys	Pro	Val	Trp	Gly	Lys	Thr	Val	Ser	Ile
	130					135					140				
Phe	Ile	Trp	Phe	Phe	Trp	Phe	Phe	Ile	Ser	Leu	Pro	Asn	Met	Ile	Leu
145					150					155					160
Ser	Asn	Lys	Glu	Ala	Thr	Pro	Ser	Ser	Val	Lys	Lys	Cys	Ala	Ser	Leu
			165						170					175	
Lys	Gly	Pro	Leu	Gly	Leu	Lys	Trp	His	Gln	Met	Val	Asn	Asn	Ile	Cys
			180					185					190		
Gln	Phe	Ile	Phe	Trp	Thr	Val	Phe	Ile	Leu	Met	Leu	Val	Phe	Tyr	Val
		195					200					205			
Val	Ile	Ala	Lys	Lys	Tyr	Met	Ile	Leu	Ile	Glu	Ser	Pro	Lys	Val	Arg
	210					215					220				
Thr	Glu	Lys	Thr	Thr	Lys	Ser	Trp	Lys	Ala	Lys	Tyr	Leu	Leu	Ser	Trp
225					230					235					240
Leu	Ser	Ser	Leu	Cys	Val	Leu	Leu	His	Phe	Ile	Ser	Pro	Glu	Phe	His
			245						250					255	
Ile	Leu	Thr	Val	Lys	Pro	Thr	Ile	Arg	Leu	Thr	Val	Asp	Cys	Lys	Ile
			260					265					270		
Asn	Cys	Leu	Leu	Leu	Lys	Lys	Gln	Leu	Ser	Phe	Trp	Gln	Gln	Leu	Thr
		275					280					285			
Phe	Val	Trp	Ile	Pro											
	290														

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 161..1192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTGGGTAT TTCTGAGAAA AAGGAAATAT TTATAAAACC ATCCAAAGAT CCAGATAATT															60
TGCAAATAAA TTGGAGGTTA TAGAGGTTAT AATCTGAATC CCAAAGGAGA CTGCAGCTGA															120
TGAAAGTGCT TCCAAACTGA AAATTGGACG TGCCTTTACG ATG GTA AGC GTT AAC															175
Met Val Ser Val Asn															
1 5															
AGC TCC CAC TGC TTC TAT AAT GAC TCC TTT AAG TAC ACT TTG TAT GGG															223
Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys Tyr Thr Leu Tyr Gly															
10 15 20															
TGC ATG TTC AGC ATG GTG TTT GTG CTT GGG TTA ATA TCC AAT TGT GTT															271
Cys Met Phe Ser Met Val Phe Val Leu Gly Leu Ile Ser Asn Cys Val															
25 30 35															
GCC ATA TAC ATT TTC ATC TGC GTC CTC AAA GTC CGA AAT GAA ACT ACA															319
Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val Arg Asn Glu Thr Thr															
40 45 50															
ACT TAC ATG ATT AAC TTG GCA ATG TCA GAC TTG CTT TTT GTT TTT ACT															367
Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu Leu Phe Val Phe Thr															
55 60 65															
TTA CCC TTC AGG ATT TTT TAC TTC ACA ACA CGG AAT TGG CCA TTT GGA															415
Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg Asn Trp Pro Phe Gly															
70 75 80 85															
GAT TTA CTT TGT AAG ATT TCT GTG ATG CTG TTT TAT ACC AAC ATG TAC															463
Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe Tyr Thr Asn Met Tyr															
90 95 100															
GGA AGC ATT CTG TTC TTA ACC TGT ATT AGT GTA GAT CGA TTT CTG GCA															511
Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala															
105 110 115															
ATT GTC TAC CCA TTT AAG TCA AAG ACT CTA AGA ACC AAA AGA AAT GCA															559
Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala															
120 125 130															
AAG ATT GTT TGC ACT GGC GTG TGG TTA ACT GTG ATC GGA GGA AGT GCA															607
Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val Ile Gly Gly Ser Ala															
135 140 145															
CCC GCC GTT TTT GTT CAG TCT ACC CAC TCT CAG GGT AAC AAT GCC TCA															655
Pro Ala Val Phe Val Gln Ser Thr His Ser Gln Gly Asn Asn Ala Ser															
150 155 160 165															
GAA GCC TGC TTT GAA AAT TTT CCA GAA GCC ACA TGG AAA ACA TAT CTC															703
Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr Trp Lys Thr Tyr Leu															
170 175 180															
TCA AGG ATT GTA ATT TTC ATC GAA ATA GTG GGA TTT TTT ATT CCT CTA															751
Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly Phe Phe Ile Pro Leu															
185 190 195															
ATT TTA AAT GTA ACT TGT TCT AGT ATG GTG CTA AAA ACT TTA ACC AAA															799
Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu Lys Thr Leu Thr Lys															
200 205 210															
CCT GTT ACA TTA AGT AGA AGC AAA ATA AAC AAA ACT AAG GTT TTA AAA															847
Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys Lys Thr Lys Val Leu Lys															

215	220	225	
ATG ATT TTT GTA CAT TTG ATC ATA TTC TGT TTC TGT TTT GTT CCT TAC Met Ile Phe Val His Leu Ile Ile Phe Cys Phe Cys Phe Val Pro Tyr 230 235 240 245			895
AAT ATC AAT CTT ATT TTA TAT TCT CTT GTG AGA ACA CAA ACA TTT GTT Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg Thr Gln Thr Phe Val 250 255 260			943
AAT TGC TCA GTA GTG GCA GCA GTA AGG ACA ATG TAC CCA ATC ACT CTC Asn Cys Ser Val Val Ala Ala Val Arg Thr Met Tyr Pro Ile Thr Leu 265 270 275			991
TGT ATT GCT GTT TCC AAC TGT TGT TTT GAC CCT ATA GTT TAC TAC TTT Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe 280 285 290			1039
ACA TCG GAC ACA ATT CAG AAT TCA ATA AAA ATG AAA AAC TGG TCT GTC Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met Lys Asn Trp Ser Val 295 300 305			1087
AGG AGA AGT GAC TTC AGA TTC TCT GAA GTT CAT GGT GCA GAG AAT TTT Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His Gly Ala Glu Asn Phe 310 315 320 325			1135
ATT CAG CAT AAC CTA CAG ACC TTA AAA AGT AAG ATA TTT GAC AAT GAA Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys Ile Phe Asp Asn Glu 330 335 340			1183
TCT GCT GCC TGA AATAAAACCA TTAGGACTCA CTGGGACAGA ACTTTCAAGT Ser Ala Ala			1235
TCCTTCAACT GTGAAAAGTG TCTTTTGGGA CAACTATTT TTCCACCTCC AAAAGAAATT AACACA			1295 1301

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys 1 5 10 15	
Tyr Thr Leu Tyr Gly Cys Met Phe Ser Met Val Phe Val Leu Gly Leu 20 25 30	
Ile Ser Asn Cys Val Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val 35 40 45	
Arg Asn Glu Thr Thr Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu 50 55 60	

Leu	Phe	Val	Phe	Thr	Leu	Pro	Phe	Arg	Ile	Phe	Tyr	Phe	Thr	Thr	Arg	65	70	75	80
Asn	Trp	Pro	Phe	Gly	Asp	Leu	Leu	Cys	Lys	Ile	Ser	Val	Met	Leu	Phe		85	90	95
Tyr	Thr	Asn	Met	Tyr	Gly	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	100	105	110	
Asp	Arg	Phe	Leu	Ala	Ile	Val	Tyr	Pro	Phe	Lys	Ser	Lys	Thr	Leu	Arg	115	120	125	
Thr	Lys	Arg	Asn	Ala	Lys	Ile	Val	Cys	Thr	Gly	Val	Trp	Leu	Thr	Val	130	135	140	
Ile	Gly	Gly	Ser	Ala	Pro	Ala	Val	Phe	Val	Gln	Ser	Thr	His	Ser	Gln	145	150	155	160
Gly	Asn	Asn	Ala	Ser	Glu	Ala	Cys	Phe	Glu	Asn	Phe	Pro	Glu	Ala	Thr	165	170		175
Trp	Lys	Thr	Tyr	Leu	Ser	Arg	Ile	Val	Ile	Phe	Ile	Glu	Ile	Val	Gly	180	185	190	
Phe	Phe	Ile	Pro	Leu	Ile	Leu	Asn	Val	Thr	Cys	Ser	Ser	Met	Val	Leu	195	200	205	
Lys	Thr	Leu	Thr	Lys	Pro	Val	Thr	Leu	Ser	Arg	Ser	Lys	Ile	Asn	Lys	210	215	220	
Thr	Lys	Val	Leu	Lys	Met	Ile	Phe	Val	His	Leu	Ile	Ile	Phe	Cys	Phe	225	230	235	240
Cys	Phe	Val	Pro	Tyr	Asn	Ile	Asn	Leu	Ile	Leu	Tyr	Ser	Leu	Val	Arg	245	250	255	
Thr	Gln	Thr	Phe	Val	Asn	Cys	Ser	Val	Val	Ala	Ala	Val	Arg	Thr	Met	260	265	270	
Tyr	Pro	Ile	Thr	Leu	Cys	Ile	Ala	Val	Ser	Asn	Cys	Cys	Phe	Asp	Pro	275	280	285	
Ile	Val	Tyr	Tyr	Phe	Thr	Ser	Asp	Thr	Ile	Gln	Asn	Ser	Ile	Lys	Met	290	295	300	
Lys	Asn	Trp	Ser	Val	Arg	Arg	Ser	Asp	Phe	Arg	Phe	Ser	Glu	Val	His	305	310	315	320
Gly	Ala	Glu	Asn	Phe	Ile	Gln	His	Asn	Leu	Gln	Thr	Leu	Lys	Ser	Lys	325	330	335	
Ile	Phe	Asp	Asn	Glu	Ser	Ala	Ala									340			

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
GACTAAAGCT TAATGAGTAG TGAAATGGTG 30
- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 31 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
GAACTTCTAG ACCCTCAGGG TTGTAAATCA G 31
- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
GACTAAAGCT TAATGAGGCC CACATGGGCA 30
- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 32 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
GAACTTCTAG ACGAACTAGT GGATCCCCC GG 32
- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
GACTAAAGCT TAATGGCGTC TTTCTCTGCT 30
- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
GAACTTCTAG ACTTCACACA GTTGTACTAT 30

(2) INFORMATION FOR SEQ ID NO:15:  
(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 30 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
GACTAAAGCT TAATGGTAAG CGTTAACAGC 30

(2) INFORMATION FOR SEQ ID NO:16:  
(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 31 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
GAACTTCTAG ACTTCAGGCA GCAGATTCAT T 31

(2) INFORMATION FOR SEQ ID NO:17:  
(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 34 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
GTCCAAGCTT GCCACCATGA GTAGTGAAAT GGTG 34

(2) INFORMATION FOR SEQ ID NO:18:  
(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 58 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGGTTGT AAATCAGG 58

(2) INFORMATION FOR SEQ ID NO:19:  
(i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 34 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
GTCCAAGCTT GCCACCATGG TTGGTGGCAC CTGG 34

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 58 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGTGGATC CCCCGTGC 58

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 34 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCCAAGCTT GCCACCATGA ACACCACAGT AATG 34

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 61 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAAGGGATC CATAAAATG 60  
T 61

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 34 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCAAGCTT GCCACCATGG TAAGCGTTAA CAGC 34

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 61 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGCAGCA GATTCATTGT 60  
C 61

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 30 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
CGGGATCCCT CCATGAGTAG TGAAATGGTG 30

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 29 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
CGGGATCCCG CTCAGGGTTG TAAATCAGG 29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 222 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Phe	Phe	Leu	Ser	His	Leu	Ala	Ile	Val	Asp	Ile	Ala	Tyr	Ala	Cys	Asn	1	5	10	15
Thr	Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Leu	Asp	Pro	Val	Lys	Pro	Ile	20	25	30	
Ser	Tyr	Ala	Gly	Cys	Met	Thr	Gln	Thr	Phe	Leu	Phe	Leu	Thr	Phe	Ala	35	40	45	
Ile	Thr	Glu	Cys	Leu	Leu	Leu	Val	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Val	50	55	60	
Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Ser	Ala	Ile	Met	Ser	Trp	Arg	Val	65	70	75	80
Cys	Ser	Thr	Met	Ala	Val	Thr	Ser	Trp	Ile	Ile	Gly	Val	Leu	Leu	Ser	85	90	95	
Leu	Ile	His	Leu	Val	Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Val	Ser	Gln	100	105	110	

Lys	Val	Asn	His	Phe	Phe	Cys	Glu	Ile	Thr	Ala	Ile	Leu	Lys	Leu	Ala	
		115					120					125				
Cys	Ala	Asp	Thr	His	Leu	Asn	Glu	Thr	Met	Val	Leu	Ala	Gly	Ala	Val	
	130					135					140					
Ser	Val	Leu	Val	Gly	Pro	Phe	Ser	Ser	Ile	Val	Val	Ser	Tyr	Ala	Cys	
145					150					155					160	
Ile	Leu	Gly	Ala	Ile	Leu	Lys	Ile	Gln	Ser	Glu	Glu	Gly	Gln	Arg	Lys	
				165					170					175		
Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Tyr	
			180					185					190			
Gly	Thr	Ala	Ile	Val	Met	Tyr	Val	Gly	Pro	Arg	His	Gly	Ser	Pro	Lys	
		195					200					205				
Glu	Gln	Lys	Lys	Tyr	Leu	Leu	Leu	Phe	His	Ser	Leu	Phe	Asn			
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Gly	Pro	Thr	Ser	Val	Pro	Leu	Val	Lys	Ala	His	Arg	Ser	Ser	Val	
1				5					10					15		
Ser	Asp	Tyr	Val	Asn	Tyr	Asp	Ile	Ile	Val	Arg	His	Tyr	Asn	Tyr	Thr	
			20					25					30			
Gly	Lys	Leu	Asn	Ile	Ser	Ala	Asp	Lys	Glu	Asn	Ser	Ile	Lys	Leu	Thr	
		35					40					45				
Ser	Val	Val	Phe	Ile	Leu	Ile	Cys	Cys	Phe	Ile	Ile	Leu	Glu	Asn	Ile	
	50					55					60					
Phe	Val	Leu	Leu	Thr	Ile	Trp	Lys	Thr	Lys	Lys	Phe	His	Arg	Pro	Met	
65					70					75					80	
Tyr	Tyr	Phe	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ala	Gly	Val	
				85					90					95		
Ala	Tyr	Thr	Ala	Asn	Leu	Leu	Leu	Ser	Gly	Ala	Thr	Thr	Tyr	Lys	Leu	
			100					105					110			
Thr	Pro	Ala	Gln	Trp	Phe	Leu	Arg	Glu	Gly	Ser	Met	Phe	Val	Ala	Leu	
		115					120					125				
Ser	Ala	Ser	Val	Phe	Ser	Leu	Leu	Ala	Ile	Ala	Ile	Glu	Arg	Tyr	Ile	
	130					135					140					

Thr	Met	Leu	Lys	Met	Lys	Leu	His	Asn	Gly	Ser	Asn	Asn	Phe	Arg	Leu	145	150	155	160
Phe	Leu	Leu	Ile	Ser	Ala	Cys	Trp	Val	Ile	Ser	Leu	Ile	Leu	Gly	Gly	165	170	175	
Leu	Pro	Ile	Met	Gly	Trp	Asn	Cys	Ile	Ser	Ala	Leu	Ser	Ser	Cys	Ser	180	185	190	
Thr	Val	Leu	Pro	Leu	Tyr	His	Lys	His	Tyr	Ile	Leu	Phe	Cys	Thr	Thr	195	200	205	
Val	Phe	Thr	Leu	Leu	Leu	Leu	Ser	Ile	Val	Ile	Leu	Tyr	Cys	Arg	Ile	210	215	220	
Tyr	Ser	Leu	Val	Arg	Thr	Arg	Ser	Arg	Arg	Leu	Thr	Phe	Arg	Lys	Asn	225	230	235	240
Ile	Ser	Lys	Ala	Ser	Arg	Ser	Ser	Glu	Asn	Val	Ala	Leu	Leu	Lys	Thr	245	250	255	
Val	Ile	Ile	Val	Leu	Ser	Val	Phe	Ile	Ala	Cys	Trp	Ala	Pro	Leu	Phe	260	265	270	
Ile	Leu	Leu	Leu	Leu	Asp	Val	Gly	Cys	Lys	Val	Lys	Thr	Cys	Asp	Ile	275	280	285	
Leu	Phe	Arg	Ala	Glu	Tyr	Phe	Leu	Val	Leu	Ala	Val	Leu	Asn	Ser	Gly	290	295	300	
Thr	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Thr	Asn	Lys	Glu	Met	Arg	Arg	Ala	305	310	315	320
Phe	Ile	Arg	Ile	Met	Ser	Cys	Cys	Lys	Cys	Pro	Ser	Gly	Asp	Ser	Ala	325	330	335	
Gly	Lys	Phe	Lys	Arg	Pro	Ile	Ile	Ala	Gly	Met	Glu	Phe	Ser	Arg	Ser	340	345	350	
Lys	Ser	Asp	Asn	Ser	Ser	His	Pro	Gln	Lys	Asp	Glu	Gly	Asp	Asn	Pro	355	360	365	
Glu	Thr	Ile	Met	Ser	Ser	Gly	Asn	Val	Asn	Ser	Ser	Ser				370	375	380	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ile	Asn	Ser	Thr	Ser	Thr	Gln	Pro	Pro	Asp	Glu	Ser	Cys	Ser	Gln	Asn	1	5	10	15
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Leu	Leu	Ile	Thr	Gln	Gln	Ile	Ile	Pro	Val	Leu	Tyr	Cys	Met	Val	Phe		
			20					25					30				
Ile	Ala	Gly	Ile	Leu	Leu	Asn	Gly	Val	Ser	Gly	Trp	Ile	Phe	Phe	Tyr		
		35					40					45					
Val	Pro	Ser	Ser	Lys	Ser	Phe	Ile	Ile	Tyr	Leu	Lys	Asn	Ile	Val	Ile		
	50					55					60						
Ala	Asp	Phe	Val	Met	Ser	Leu	Thr	Phe	Pro	Phe	Lys	Ile	Leu	Gly	Asp		
65					70					75					80		
Ser	Gly	Leu	Gly	Pro	Trp	Gln	Leu	Asn	Val	Phe	Val	Cys	Arg	Val	Ser		
				85					90					95			
Ala	Val	Leu	Phe	Tyr	Val	Asn	Met	Tyr	Val	Ser	Ile	Val	Phe	Phe	Gly		
			100					105					110				
Leu	Ile	Ser	Phe	Asp	Arg	Tyr	Tyr	Lys	Ile	Val	Lys	Pro	Leu	Trp	Thr		
		115					120					125					
Ser	Phe	Ile	Gln	Ser	Val	Ser	Tyr	Ser	Lys	Leu	Leu	Ser	Val	Ile	Val		
	130					135					140						
Trp	Met	Leu	Met	Leu	Leu	Leu	Ala	Val	Pro	Asn	Ile	Ile	Leu	Thr	Asn		
145					150					155					160		
Gln	Ser	Val	Arg	Glu	Val	Thr	Gln	Ile	Lys	Cys	Ile	Glu	Leu	Lys	Ser		
				165					170					175			
Glu	Leu	Gly	Arg	Lys	Trp	His	Lys	Ala	Ser	Asn	Tyr	Ile	Phe	Val	Ala		
			180					185					190				
Ile	Phe	Trp	Ile	Val	Phe	Leu	Leu	Leu	Ile	Val	Phe	Tyr	Thr	Ala	Ile		
		195					200					205					
Thr	Lys	Lys	Ile	Phe	Lys	Ser	His	Leu	Lys	Ser	Ser	Arg	Asn	Ser	Thr		
	210					215					220						
Ser	Val	Lys	Lys	Lys	Ser	Ser	Arg	Asn	Ile	Phe	Ser	Ile	Val	Phe	Val		
225					230					235					240		
Phe	Phe	Val	Cys	Phe	Val	Pro	Tyr	His	Ile	Ala	Arg	Ile	Pro	Tyr	Thr		
				245					250					255			
Lys	Ser	Gln	Thr	Glu	Ala	His	Tyr	Ser	Cys	Gln	Ser	Lys	Glu	Ile	Leu		
			260					265					270				
Arg	Tyr	Met	Lys	Glu	Phe	Thr	Leu	Leu	Leu	Ser	Ala	Ala	Asn	Val	Cys		
		275					280					285					
Leu	Asp	Pro	Ile	Ile	Tyr	Phe	Phe	Leu	Cys	Gln	Pro	Phe	Arg	Glu	Ile		
	290					295					300						
Leu	Cys	Lys	Lys	Leu	His	Ile	Pro	Leu	Lys	Ala	Gln	Asn	Asp	Leu	Asp		
305					310					315					320		
Ile	Ser	Arg	Ile	Lys													
				325													

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser	Ser	Asn	Cys	Ser	Thr	Glu	Asp	Ser	Phe	Lys	Tyr	Thr	Leu	Tyr	Gly	
1				5					10					15		
Cys	Val	Phe	Ser	Met	Val	Phe	Val	Leu	Gly	Leu	Ile	Ala	Asn	Cys	Val	
			20					25					30			
Ala	Ile	Tyr	Ile	Phe	Thr	Phe	Thr	Leu	Lys	Val	Arg	Asn	Glu	Thr	Thr	
		35					40					45				
Thr	Tyr	Met	Leu	Met	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Val	Phe	Thr	
	50					55					60					
Leu	Pro	Phe	Arg	Ile	Tyr	Tyr	Phe	Val	Val	Arg	Asn	Trp	Pro	Phe	Gly	
65				70						75					80	
Asp	Val	Leu	Cys	Lys	Ile	Ser	Val	Thr	Leu	Phe	Tyr	Thr	Asn	Met	Tyr	
				85					90					95		
Gly	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	Asp	Arg	Phe	Leu	Ala	
			100					105					110			
Ile	Val	His	Pro	Phe	Arg	Ser	Lys	Thr	Leu	Arg	Thr	Lys	Arg	Asn	Ala	
		115					120					125				
Arg	Ile	Val	Cys	Val	Ala	Val	Trp	Ile	Thr	Val	Leu	Ala	Gly	Ser	Thr	
	130					135					140					
Pro	Ala	Ser	Phe	Phe	Gln	Ser	Thr	Asn	Arg	Gln	Asn	Asn	Thr	Glu	Gln	
145					150					155					160	
Arg	Thr	Cys	Phe	Glu	Asn	Phe	Pro	Glu	Ser	Thr	Trp	Lys	Thr	Tyr	Leu	
				165					170					175		
Ser	Arg	Ile	Val	Ile	Phe	Ile	Glu	Ile	Val	Gly	Phe	Phe	Ile	Pro	Leu	
			180					185					190			
Ile	Leu	Asn	Val	Thr	Cys	Ser	Thr	Met	Val	Leu	Arg	Thr	Leu	Asn	Lys	
		195					200					205				
Pro	Leu	Thr	Leu	Ser	Arg	Asn	Lys	Leu	Ser	Lys	Lys	Lys	Val	Leu	Lys	
	210					215					220					
Met	Ile	Phe	Val	His	Leu	Val	Ile	Phe	Cys	Phe	Cys	Phe	Val	Pro	Tyr	
225					230					235					240	
Asn	Ile	Thr	Leu	Ile	Leu	Tyr	Ser	Leu	Met	Arg	Thr	Gln	Thr	Trp	Ile	
				245					250					255		
Asn	Cys	Ser	Val	Val	Thr	Ala	Val	Arg	Thr	Met	Tyr	Pro	Val	Thr	Leu	



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			260						265					270			
Cys	Ile	Ala	Val	Ser	Asn	Cys	Cys	Phe	Asp	Pro	Ile	Val	Tyr	Tyr	Phe		
		275					280					285					
Thr	Ser	Asp	Thr	Asn	Ser	Glu	Leu	Asp	Lys	Lys	Gln	Gln	Val				
	290					295					300						